

Project Epsilon progress report

The Neural Basis of Loss Aversion in Decision-Making Under Risk

Jo, Min Gu
mingujo

Kaam, Soazig
soazig

Li, Zhuangdi
lizhua

Yu, Timothy
timothy1191xa

Zhi, Ye
ye-zhi

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1 Abstract

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2 Introduction

The study *Neural Basis of Loss Aversion in Decision-Making Under Risk* [1] focuses on decision-making process, especially on the correlation between the neural activity and the reluctance to lose. 16 people were presented 255 gambling situations with a 50% of success. Each situation was associated with a potential gain and loss that were randomly selected. The gains were ranging from \$10 to \$40 while the losses from \$5 to \$20. The participants were asked to assess their level of willingness to accept or reject the gamble using a 4-point likert scale [1: strongly accept, 2: weakly accept, 3: weakly reject, 4:strongly reject]. The response time was also recorded for each case. The imaging data were collected using the fMRI method. They were processed and analyzed in order to identify the regions of the brain activated by the decision making process. This study also investigated the relationship between the brain activity and the behavior of the subjects towards the gambling situations using a whole-brain robust regression analysis.

3 Data

3.1 Description the data

The data we are using can be found on the OpenfMRI website at the following address: <https://www.openfmri.org/dataset/ds000005>, the dsnum is ds005. For our project, we are specifically using the behavior data and the BOLD data that are organized.

For each of runs per subject (3), the behavior data contains the timestamp of each survey question (onset), the gain/loss combinations (gain and loss), the response for the particular trial (respnum) from the 4-point likert scale. The researcher created a response category (respcat) to be used in their binary choice model that combines the “reject” answers together on one hand and the “accept” answers together on the other hand. BOLD data contains compressed 4-dimensional brain images for each subject’s run. The folder also comports Quality Assurance (QA) files and a report.

Thanks to the resampling method and templates made available by the the Montreal Neurological Institute, filtered have also been provided. The files have been resampled to a normalized 2mm voxel sizes. This standardization method of the brain will allow us to perform cross subject or cross run analyses.

3.2 Exploratory Analysis

We explore the data by reproducing some provided figures from the QA report and provided by the OpenfMRI researchers. The Figures 1 and 2 show the transversal slices of brain images with the mean values of the voxels accross time.

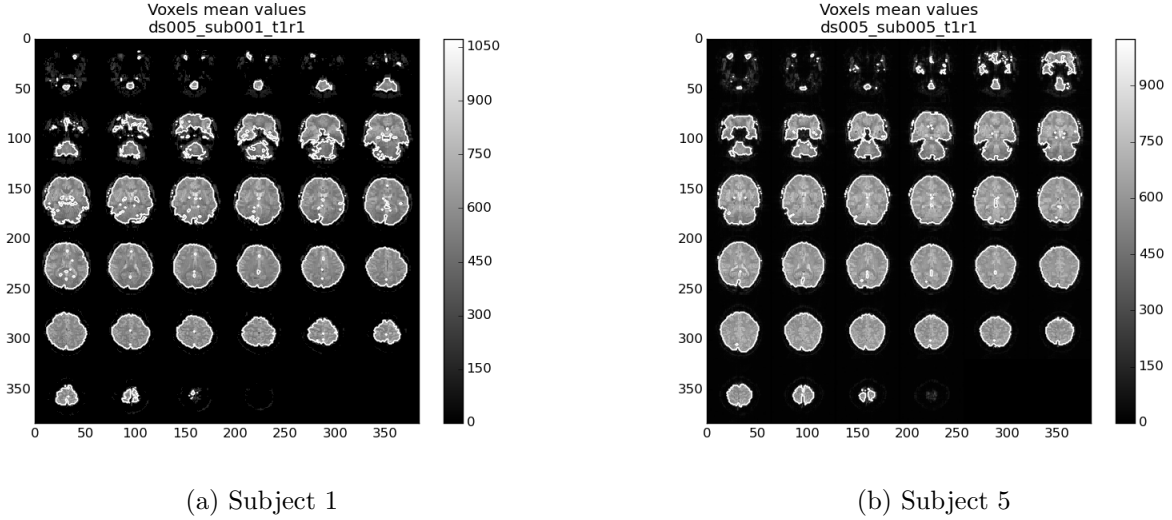


Figure 1: Mean value of the voxels accross time for the 34 slices of the transversal cut of the brain raw data for subject 1 and subject 5

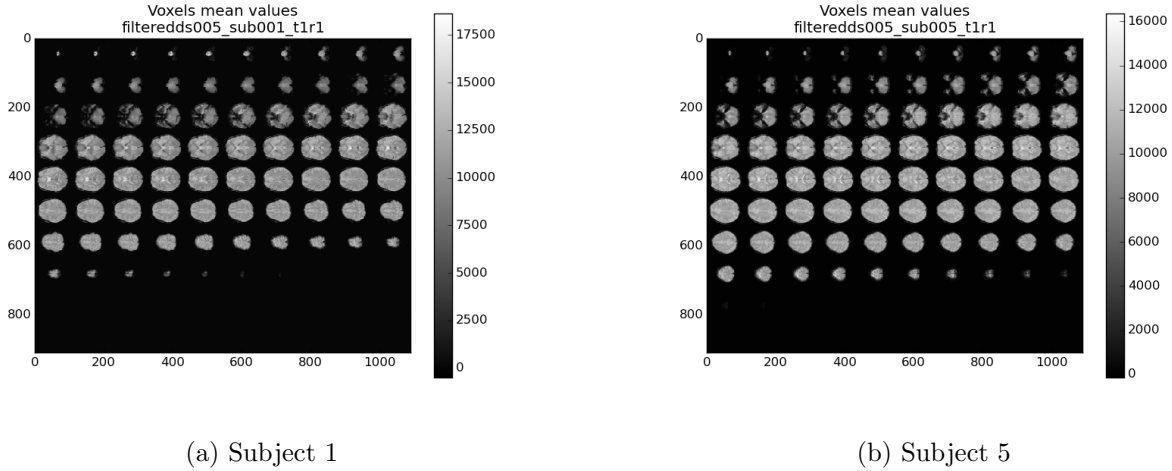
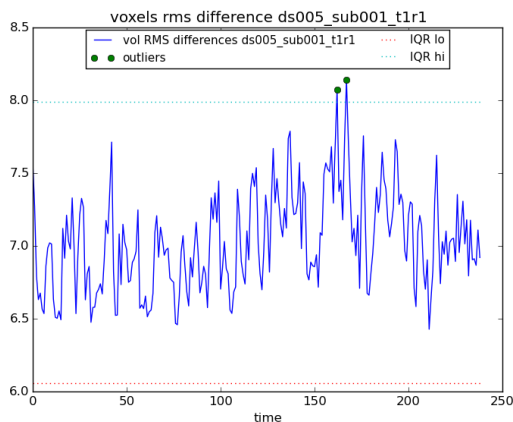
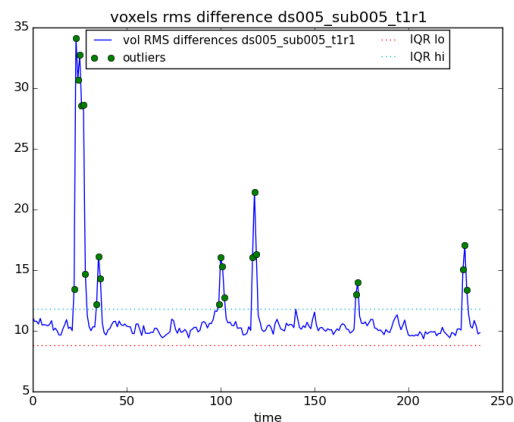


Figure 2: Mean value of the voxels accross time for the 91 slices of the transversal cut of the brain filtered data for subject 1 and subject 5

In Figure 3, we visualize the root mean square difference across time between for the 1rst run of subecjt 1 and 5. As we expected, there is variations in the voxels volumes accross time. The noise correction is addressed in the BOLD image analysis section. These graphs also show that there is a big difference in 'mean brain activation' accross subject. We will explore these differences that can be tied to behavioral data as seen in the next section.



(a) Subject 1



(b) Subject 5

Figure 3: Voxels time course root mean square for subject 1 and 5 - run 1

4 Behavioral Data Analysis

4.1 Introduction

First of all, we generated some summary statistics including correlation among variables, and tried both linear and logistic regression analysis for behavioral data. The scientific questions that we have are - if we can explain response (to gamble or not to gamble) based on the gain and loss.

4.2 Methods

We did some explanatory data analysis and regression analysis using behavior data. For explanatory data analysis, we generated some summary statistics, including correlation among variables and simple plots to better understand the behavior. And then we used regression analysis to mainly answer two scientific questions. The scientific questions that we have are:

- If gain/loss would be significant for individuals who choose to participate and how much time it would take for them to respond.
- If gain/loss would be significant for whether individuals would like to participate in the gamble.

4.2.1 Linear Regression

I will change this.

1. Response Time \sim gain + loss
2. Response Time \sim diff(gain-loss)
3. Response Time \sim ratio(gain/loss)

4.2.2 Logistic Regression

Logistic Regression is a statistical technique capable of predicting a binary outcome. Since, in this data, the researchers classify the decision to gamble as 1 (gamble) or 0 (not gamble), we can use logistic regression technique to explain the subject's tendency to gamble or not based on the condition of the gain and loss amount given in the process of experiment. Our goal is to identify how gain and loss amount influence each subject's response. To do this, we use the statsmodels Logit function. We specify the response column in the behavior txt file as the one containing the variable we're trying to explain and the gain and loss columns as the predictor variables. After plotting the results on the plot, we were able to see some interesting behaviors of some subjects. As you see from the plot, Subject 1 is in general more risk seeking: as long as the gain amount is large enough as 20 dollars, he decides to gamble. However, Subject 3 shows the opposite behavior: she does not participate in the gamble when her loss amount is higher than 10 dollars no matter what the gain amount is. (To see the overall behaviors from all subjects, see the appendix) Overall, we could see that the logistic regression line fits well on the border between the decision to gamble and not gamble.

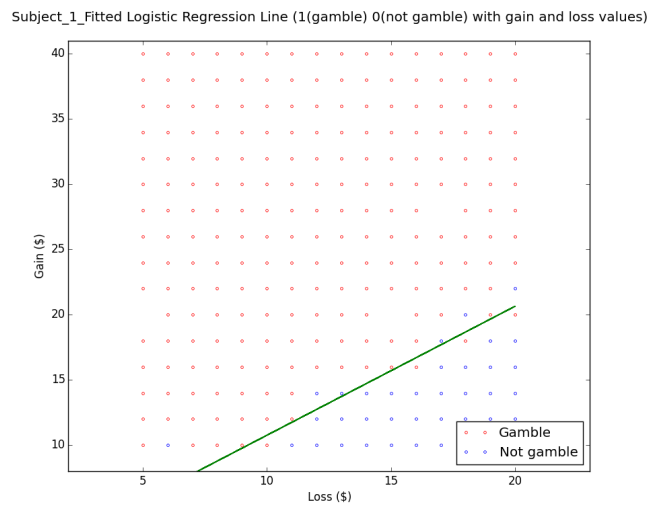


Figure 4: Fitted Logistic Regression line on subject 1's behavior data (predictors gain, loss)

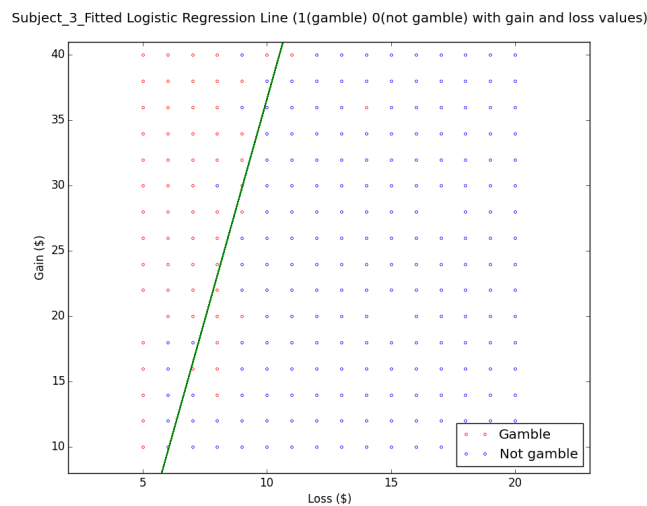


Figure 5: Fitted Logistic Regression line on subject 3's behavior data (predictors gain, loss)

4.3 Results

For linear regression, ratio is a significant predictor and people would actually care more about loss than gain.

The paper illustrates as people typically reject gambles that offer a 50/50 chance of gaining or losing money, unless the amount that could be gained is at least twice the amount that could be lost (Sabrina). In the experiment, the given gain and loss amount ratio to each subject is around 2 to 1. This refers subjects would not merely show risk averse behavior every trial. We could confirm this trend by observing the plots. We are hard to tell whether subjects are risk averse or not.

5 Image Data Analysis

5.1 Introduction

After exploring behavior data, we proceed to image data analysis. First we need to apply convolution to connect behavior stimuli and neural activity. Then we can run general linear regression to find activated voxels across time course. Using hypothesis testing, we can actually locate and visualize the activated voxels. After finishing basic steps, we try to apply noise modeling and PCA to compare the MRSS so that we can finally decide our design matrix.

5.2 Methods

Here are some of the methods (this needs to be updated soon as well.)

5.2.1 Convolution

Our experiment is event-oriented. The subject is shown with the different conditions such as gain and loss amounts over random time. After being provided with the conditions, the blood flow responses starts to fluctuate. To predict the fMRI signal to an event, we need to predict the hemodynamic responses to neural activity. A predictor neural time course is typically obtained by convolution of a condition of the experiment with a standard hemodynamic response function. With this predictor, we build our design matrix for our general linear model on each voxel of a subject's brain. To produce such predictor, we practiced two different approaches.

- Convolution with canonical HRF

A typical BOLD response to a single, impulsive stimulation resembles a linear combination of two Gamma function. This would model a signal is instantly at its peak level at the onset of a given condition and instantly undershoot back to around baseline with the offset of a condition. We can use this hemodynamic response function as a canonical one. Generally, the canonical HRF should be a good fit if we believe the subjects to be normal in many cortical regions. Using this canonical HRF will help us to find how much the canonical HRF has to be scaled enough to account for the signal. However, we want to be more in detail as long as

1. The onsets of the HRF can happen in the middle of volumes due to the conditions given at different times.
2. The amplitudes vary according to the parametric gain and loss conditions. Thus, the true shape of HRF for each subject should vary.

- Convolution at finer time resolution

Therefore, we would make a neural and hemodynamic regressor at a finer time resolution than the TRs, and later sample this regressor at the TR onset times. This refers that stimulus onsets do not have to be synchronized with scan TRs.

– Result

To analyze the difference between two approaches, we compare the MRSS from two linear regressions on image data of three subjects (1,2,3) using convolution predictors from two different approaches. In the below table, we see the MRSS from linear regression using the latter approach has slightly lower residuals compared to the former method. This makes sense because, using the latter method, we are able to more elaborately preprocess the data.

5.2.2 GLM

The first matrix we get from convolution has five columns, which correspond to a column of ones and 4 cond.txt files in our dataset, respectively. After we get the convolution matrix, we use it as our design matrix to run the generalized linear regression on the image data. The dimension of our data is (64, 64, 34, 240), so, first we reshape our data into 2 dimensional array, which has the shape of (64*64*34, 240); the first dimension corresponds to 3-dimensional voxel indices and the second dimension corresponds to the time slice. Then we pass our design matrix into the glm function to calculate the related beta hats. Thus, there are in total 139624 beta hats that we get from the regression correspond to the first three dimensions of our image data. For example, the first beta hat contains the information about the voxel (0,0,0). Then we turn the beta hats back into 4-dimensional shape and run the diagnostic functions on the 4-d beta hats. Based on the predictors, we can calculate the fitted values and then the residuals. We use the MRSS of the first three dimensions as a measurement of our regression; in general, a smaller MRSS indicates a better performance of the regression model.

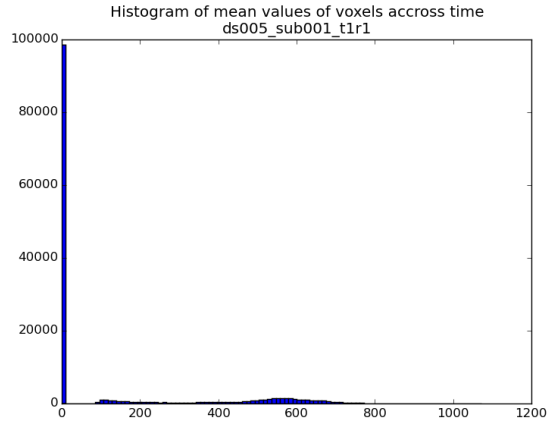
5.2.3 Smoothing

After we tried with the normal convolution matrix, we also generated high resolution convolution matrix and used it for linear regression. It turned out that the MRSS is just reduced by a little bit. Then we write a smoothing function to implement the multidimensional Gaussian filter on our data. We repeat the same procedures as what we have done in normal convolution on the smoothed data and the MRSS are reduced sharply. Therefore, we concluded that the smoothing method is a good pre-processing when we do the linear regression.

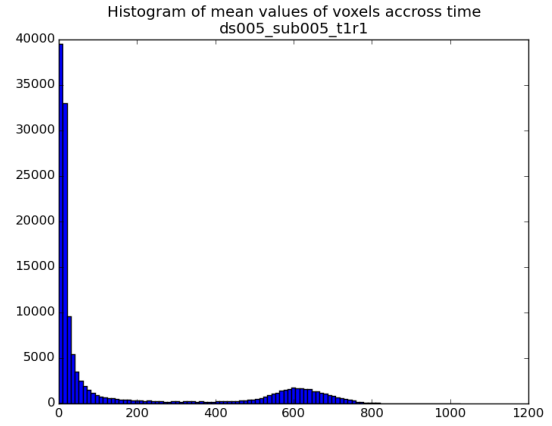
6 Noise modeling

6.1 In brain voxels

For our analysis, we use the voxel by time matrix that only includes the voxel inside of the brain. For the raw data, we determine the mask visually by plotting the histogram of the mean values of the voxels across time.



(a) Subject 1



(b) Subject 5

Figure 6: Histogram of mean value of the voxels across time for subject 1 and 5 - run 1

We can see from Figure ?? and ?? for the first run for subjects 1 and 5 that we can set the threshold to a mean value of the voxels across time of 375. Our further analysis with the raw data uses a mask on the mean data across time that selects the ones with a higher value than the threshold.

6.2 Selecting the voxels in the brain - filtered data

For the filtered data, we applied the mask provided by the Montreal Neurological Institute's website. The filter has 1 for the voxels inside the brain and 0 outside. We created a function in the 'project-epsilon/code/utis/scripts' directory to apply the mask on these provided filtered data. The function also saves a .nib file in the same directory as the filtered data.

6.3 Linear and quadratic drifts

In our quality control analysis, we were interested to remove the noise from the BOLD images. The previous section explained how we select the voxels that are in the brain. This section is dealing with noise motion.

Applying the mask on the image data allows us to select only the voxels that are in the brain. We then model our signal with some additional drift terms to account for the subject head motion in the scanner. We decide to add a linear and a quadratic drift terms as regressors. The following brain images justify our design decision.

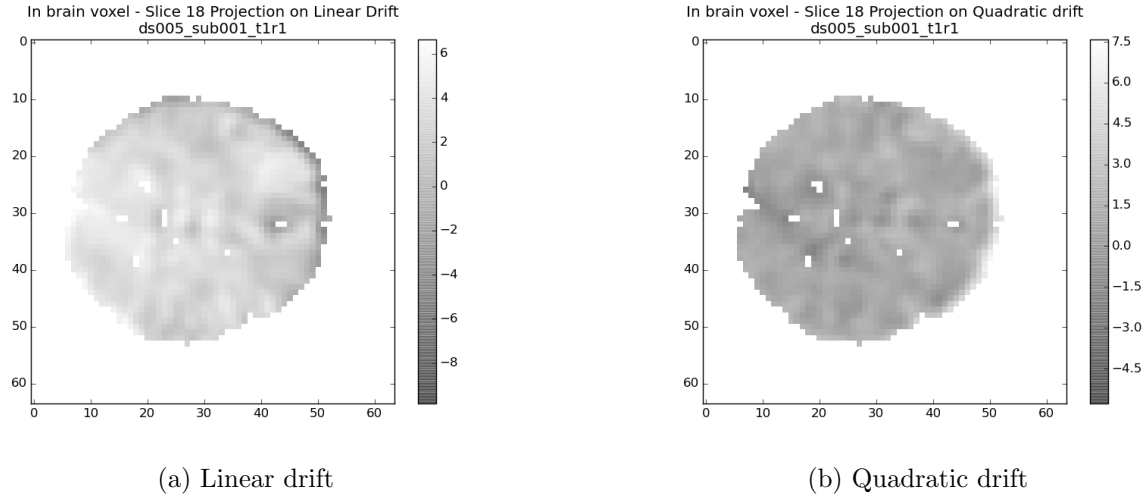


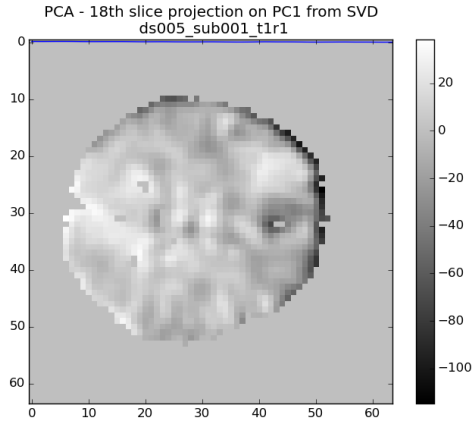
Figure 7: Projection of the brain image on the drift regressors - subject1 - run1

The above image illustrates the effect of the linear drift regressor on the BOLD image. Lighter pixels indicate a higher position of the zone compare to darker zones. We can clearly see the edges of the top right of the brain to be dark (black) and the edges on the bottom left of the brain to be light (white). This suggests a clear linear movement of the head in the direction of the axis.

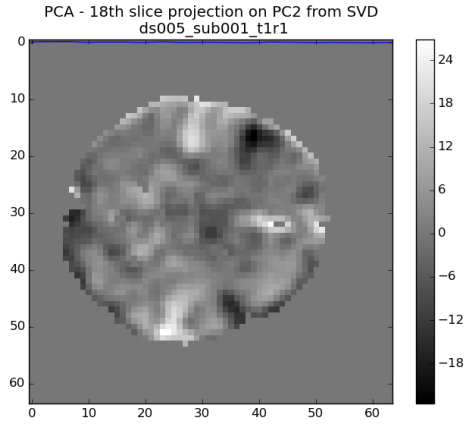
The above image clearly illustrates a strong influence on the quadratic regressor in the design matrix. We can clearly distinguish light and dark areas on the above images. Our design matrix includes the above drift regressors in order to get a more accurate estimation of the activation of the task which effects will not be confounded with the motion of the brain. The drift terms model gradual drifts across the time-series, but other parameters can explain the variance in the data. The next section is aiming to find the principal components of the data that have the most variance.

6.4 Principal Component Analysis

We substracted the mean accross voxels from our data in order to normalize the data. We then apply the Single Value Decomposition (SVD) on the covariance matrix. The resulting principal components are ordered according to the variance they explain in the data. The first principal component will be responsible for more variability than the second. Our first approach is to vizualised the projection of the voxel by time matrix onto the principal components. In Figure 8 we give then example of the run 1 of the subject 1.



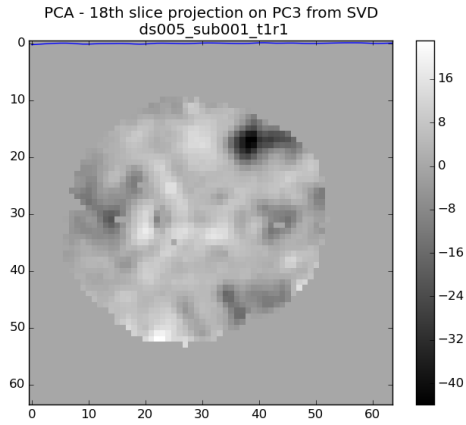
(a) First principal component - PC1



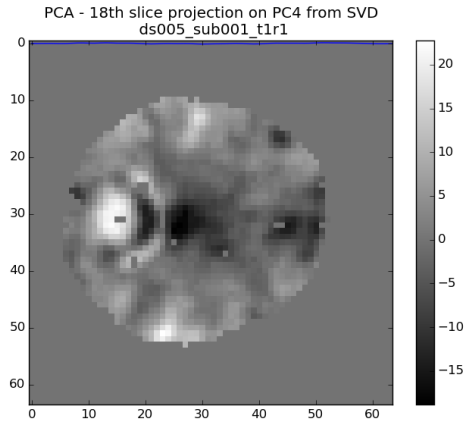
(b) Second principal component = PC2

Figure 8: Brain data projected onto principal components of the data - subject 1 - run 1

The two images above, show that distinct localization of the voxels at the edges of the brain, which suggests that they reflect brain anatomy rather than activation. We decided to remove these components by regression because they are likely to be related to noise from the scanner or the subject.



(a) Third principal component - PC3



(b) Fourth principal component = PC4

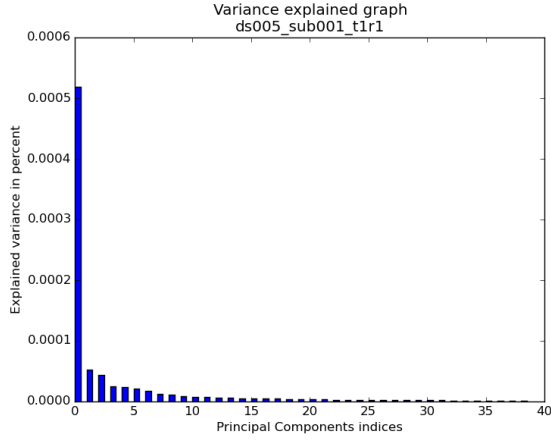
Figure 9: Brain data projected onto the principal components of the data- subject 1 - run 1

Contrary to the precedent cases, the above two images of the data onto the 3rd and 4th principal component don't seem to reveal any random pattern. The projection on the 4th is even component show a darker area localized on the striatum, region of interest for our analysis.

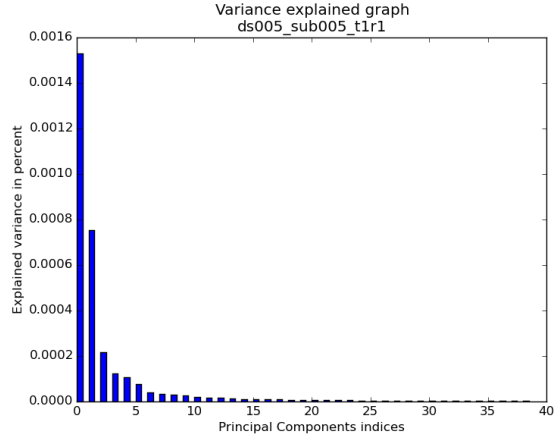
A visual analysis is always difficult to perform to select the principal components. In order to determine how many principal components to include in our design matrix, we plotted Variance Explained plots presented in the following sections.

6.5 Variance explained

In the Single Value Decomposition of the data, the the square roots of the singular values ordered from greatest to least along its diagonal. Each value indicates the variance of the component vector (time-course) along each principal component.



(a) Subject 1



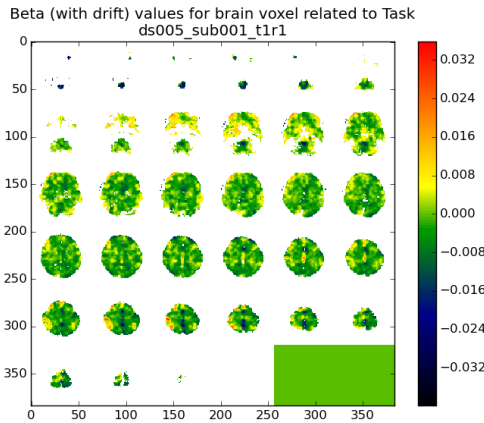
(b) Subject 5

Figure 10: Explained variance for the first [2-40] principal components of the data for subjects 1 and 5 - run 1 (the first component is not plotted for better clarity)

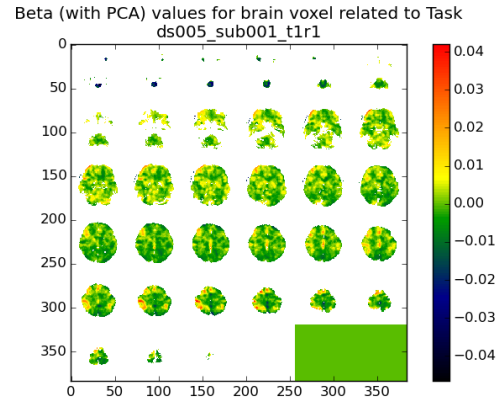
In the Figure 10, we plotted the variance associated with each principal components of the data. The first principal component accounts for more than 99percent of the overall variability. This is probably due to the high variability over time we did not account for in the design of the PCA analysis. we decided to remove the first component from the following graph for better clarity. In this particular case, the elbow shape of the graph makes a distinction between the three first (the figure does not show the first principal component). Filtering out the first three principal components is justified here.

6.6 Noise modeling results

We calculated the Mean Root Sum Square (MRSS) of the residuals of our different model. For the run 1 of the subject 1, the mean of MRSS accross the voxels decreased from 23.89 including only the drift terms to 7.32 with the inclusion of the three first principal components. We also performed the same modeling of the design matrix with the filtered data. The mean MRSS resulting is 1.04 when we include the drift terms and 0.79 including the principal components.



(a) Design matrix includes linear and quadratic drifts regressors



(b) Design matrix includes drifts and PC regressors

Figure 11: Mean values of the Betas coefficients on the slice 18 of in brain voxels

Betas coefficients of our linear model related to the brain activation with the task are plotted on the

brain image in Figure 11. We can see on both model (with or without the PC) we can localized the region of the brain related to the task activation thanks to the values of the betaghest the values are in red, the lowest in blue. From the journal article, we know the regions of interest are the inferior/middle frontal (see (100,200:400) and (150,0:300)), the ventral stratum (275, (150:400)) for example. Further analysis and statistical tests are needed to locate the activated voxels with task, which is developed in the next section.

6.6.1 Hypothesis Testing

From linear regression, we can get t-statistics for different conditions(task on/off, gain, loss, d is-
tance).For each condition, we will have a 3D t-statistics matrix. For visualization, we first ad ded mask
based the mean voxel and the histogram. We set a boolean mask which takes larger than 375 . Also we
used smooth function and better color txt to generate a better image. Then we plotted t he t statistics
map for gain/loss.

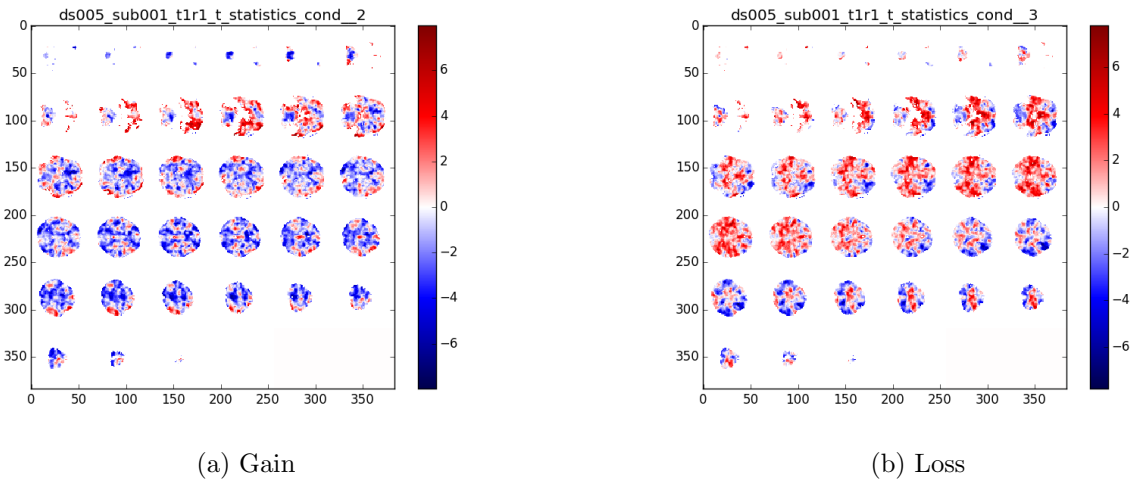


Figure 12: t statistics map for gain/loss (subject1)

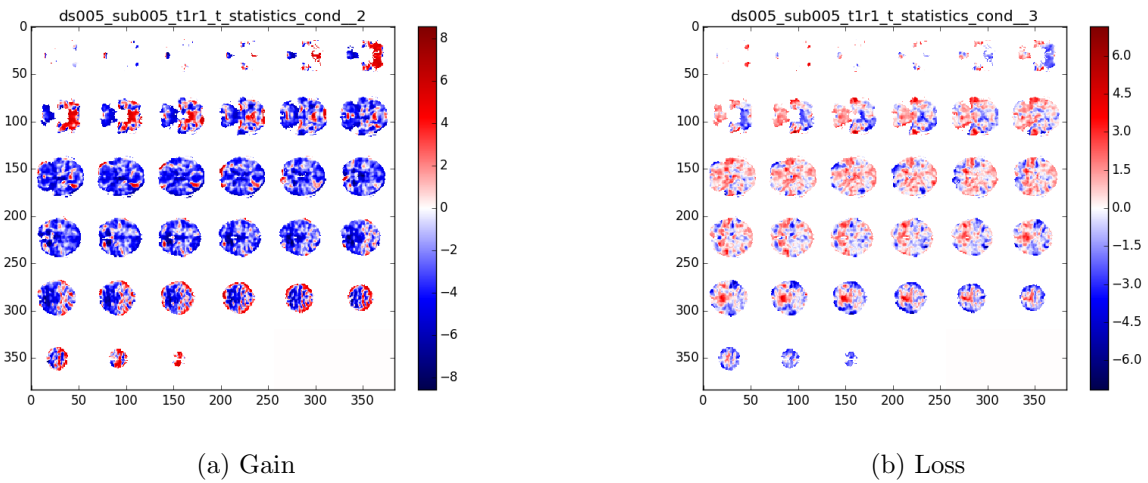


Figure 13: t statistics map for gain/loss (subject5)

The larger the t-statistics, the more significant. Thus the red spots represents the activa ted voxels for gain
and loss. For subject 1, gain has more activated voxels. However, for su bject 5, loss has more activated

voxels.

7 Multi-Comparison

7.1 Introduction

As our intended goal of this project is to locate the ROI (Region of Interest) in a brain according to this mixed gamble task, the significant issue is the specification of an appropriate threshold for statistical maps. Therefore, we are interested in multi-comparison across subjects. In the previous analysis on single subject, we were able to locate the generally activated voxels. With these data, we attempted to find out the general pattern in each voxel of brains across 16 subjects.

7.2 Methods

As our intended goal of this project is to locate the ROI (Region of Interest) in a brain according to this mixed gamble task, the significant issue is the specification of an appropriate threshold for statistical maps. Therefore, we are interested in multi-comparison across subjects. In the previous analysis on single subject, we were able to locate the generally activated voxels. With these data, we attempted to find out the general pattern in voxels of brains across 16 subjects.

To multi-compare, we chose to explore on filtered data set (shape: 91*109 * 91) since original data set is not normalized in terms of voxel location. Applying our general linear modeling on each subject as above, we first collected all beta values for each voxel across time course of each subject. Now, we have beta values of shape of (91, 109, 91) for each of 16 subjects. We compare on each single voxel across subjects. To do this, We have total 4 steps.

- Calculate average of beta value on a single voxel across 16 subjects. Do this for whole voxels.
- Calculate standard deviation of beta value on a single voxel across 16 subjects. Do this for whole voxels.
- Calculate T-statistics of beta value on a single voxel across 16 subjects. Do this for whole voxels.

$$t - statistics = \frac{\frac{mean}{SE(mean)}}{\sqrt{n}}$$

- Calculate P-value of beta value on a single voxel across 16 subjects. Do this for whole voxels.

For the 4th step, we have an issue of false positives: since we're executing 9110991 number of hypothesis testing, note that an error probability of p value = 0.05 means that if we would repeat the same test 1000 times and assume that there is no effect of the experiment, we would wrongly reject or accept the null or alternative hypothesis on average. Therefore, we decided to strengthen our p-value threshold with Bonferroni correction: our new p-value threshold is 0.05/(9110991)

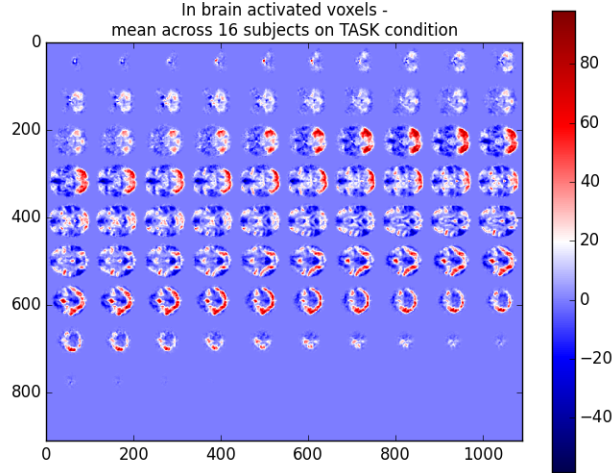


Figure 14: Mean beta values on each voxel across 16 subjects on TASK condition

7.3 Results

As the image of mean of beta values on each voxel across all subjects on task condition indicates, we are able to classify which portion of brain is in general activated due to this experiment. However, there should be fluctuation over different subjects. To identify this, standard deviation is also shown. As the image in the appendix illustrates, fluctuation occurs on similar regions because each subject's hemodynamic response degree must be different. We found out that the t-statistics in general are not significant enough; therefore, we could not elaborately indicate the specific portion of brain related to the mixed gamble task. However, t-statistics and p-value of voxels over a brain well correspond to each other.

8 Discussion and Conclusion

8.1 Discussion

8.2 Conclusion

Update the conclusion!

9 Appendix

9.1 Logistic Regression on Behavior Data

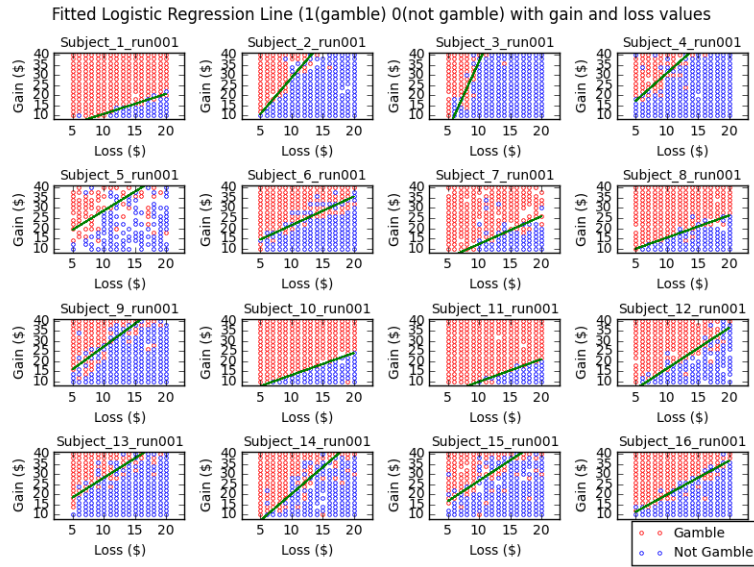


Figure 15: Logistic Regression on each subjects' behavior data

9.2 Multi-comparison across 16 subjects on TASK condition

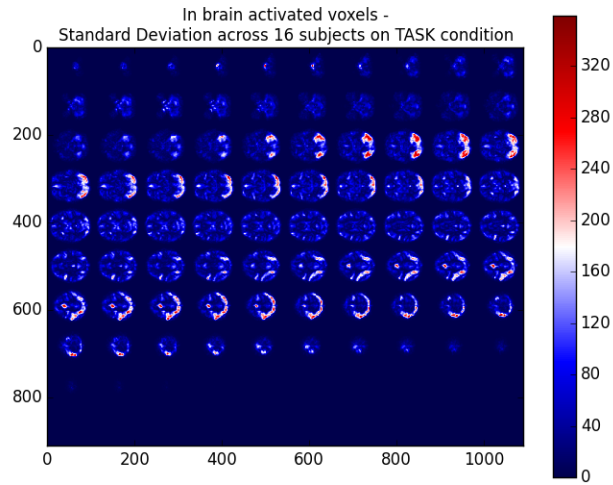


Figure 16: Standard Deviation of beta values on each voxel across 16 subjects on TASK condition

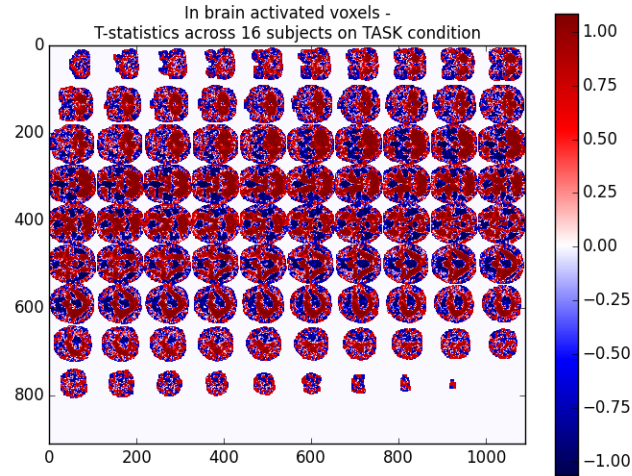


Figure 17: T-statistics of beta values on each voxel across 16 subjects on TASK condition

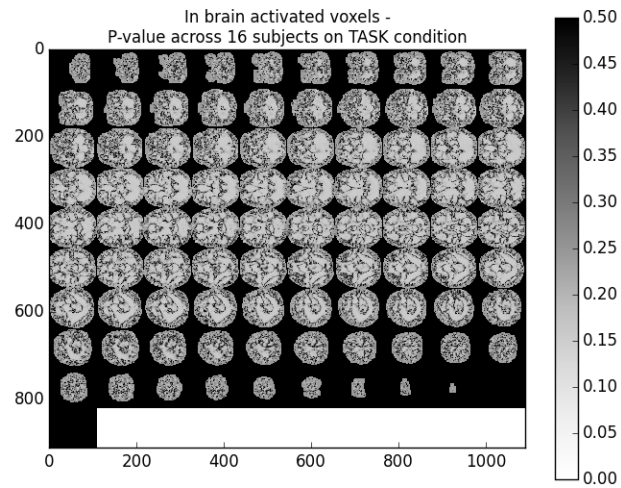


Figure 18: P-value of on each voxel across 16 subjects on TASK condition

Example 1: Multi-comparison across subjects on TASK condition. P-value indicates the porton of activated voxels

9.3 Resource2

9.4 Resource3

References

- [1] S. M. TOM, C. R. FOX, C. TREPEL, AND R. A. POLDRACK, *The neural basis of loss aversion in decision-making under risk*, Science, 315 (2007), pp. 515–518.